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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/955,572CDATE: 02/28/2000
TIME: 15:36:25

Input Set: H955572C.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

ENTERED

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1 <110> APPLICANT: Kwon, Byoung
2 <120> TITLE OF INVENTION: NEW RECEPTOR AND RELATED PRODUCTS AND
3 METHODS
4 <130> FILE REFERENCE: 740.013US2
5 <140> CURRENT APPLICATION NUMBER: US/08/955,572C
6 <141> CURRENT FILING DATE: 1997-10-22
7 <150> EARLIER APPLICATION NUMBER: 08/461,652
8 <151> EARLIER FILING DATE: 1995-06-05
9 <150> EARLIER APPLICATION NUMBER: 08/122,796
10 <151> EARLIER FILING DATE: 1993-09-03
11 <160> NUMBER OF SEQ ID NOS: 12
12 <170> SOFTWARE: FastSEQ for Windows Version 3.0
13 <210> SEQ ID NO 1
14 <211> LENGTH: 838
15 <212> TYPE: DNA
16 <213> ORGANISM: Homo sapiens
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19 catagtagcc actctgttgc tggtcctcaa ctttgagagg acaagatcat tgcaggatcc 120
20 ttgtagtaac tgcccagctg gtacattctg tgataataac aggaatcaga tttgcagtcc 180
21 ctgtcctcca aatagtttct ccagcgcagg tggacaaagg acctgtgaca tatgcaggca 240
22 gtgtaaaggt gttttcagga ccaggaagga gtgttcctcc accagcaatg cagagtgtga 300
23 ctgcactcca gggtttcact gcctgggggc aggatgcagc atgtgtgaac aggattgtaa 360
24 acaagggtcaa gaactgacaa aaaaagggtg taaagactgt tgctttggga catttaacga 420
25 tcagaaacgt ggcattctgc gacctggac aaactgttct ttggatggaa agtctgtgct 480
26 tgtgaatggg acgaaggaga gggacgtggt ctgtggacca tctccagctg acctctctcc 540
27 gggagcatcc tctgtgaccc cgctgcccc tgcgagagag ccaggacact ctccgcagat 600
28 catctccttc tttcttgccg tgacgtcgac tgcgttgctc ttctgtctgt tcttcctcac 660
29 gctccgtttc tctgttggtt aacggggcag aaagaaactc ctgtatatat tcaaacaacc 720
30 atttatgaga ccagtacaaa ctactcaaga ggaagatggc tgtagctgcc gatttccaga 780
31 agaagaagaa ggaggatgtg aactgtgaaa tggaagtcaa tagggctgtt gggacttt 838
32 <210> SEQ ID NO 2
33 <211> LENGTH: 255
34 <212> TYPE: PRT
35 <213> ORGANISM: Homo sapiens
36 <400> SEQUENCE: 2
37 Met Gly Asn Ser Cys Tyr Asn Ile Val Ala Thr Leu Leu Leu Val Leu
38 1 5 10 15
39 Asn Phe Glu Arg Thr Arg Ser Leu Gln Asp Pro Cys Ser Asn Cys Pro
40 20 25 30
41 Ala Gly Thr Phe Cys Asp Asn Asn Arg Asn Gln Ile Cys Ser Pro Cys
42 35 40 45
43 Pro Pro Asn Ser Phe Ser Ser Ala Gly Gly Gln Arg Thr Cys Asp Ile
44 50 55 60
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45      Cys Arg Gln Cys Lys Gly Val Phe Arg Thr Arg Lys Glu Cys Ser Ser
46      65                               70                               75                               80
47      Thr Ser Asn Ala Glu Cys Asp Cys Thr Pro Gly Phe His Cys Leu Gly
48                               85                               90                               95
49      Ala Gly Cys Ser Met Cys Glu Gln Asp Cys Lys Gln Gly Gln Glu Leu
50                               100                              105                              110
51      Thr Lys Lys Gly Cys Lys Asp Cys Cys Phe Gly Thr Phe Asn Asp Gln
52                               115                              120                              125
53      Lys Arg Gly Ile Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Lys
54                               130                              135                              140
55      Ser Val Leu Val Asn Gly Thr Lys Glu Arg Asp Val Val Cys Gly Pro
56      145                               150                               155                               160
57      Ser Pro Ala Asp Leu Ser Pro Gly Ala Ser Ser Val Thr Pro Pro Ala
58                               165                               170                               175
59      Pro Ala Arg Glu Pro Gly His Ser Pro Gln Ile Ile Ser Phe Phe Leu
60                               180                              185                              190
61      Ala Leu Thr Ser Thr Ala Leu Leu Phe Leu Leu Phe Phe Leu Thr Leu
62                               195                              200                              205
63      Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
64      210                               215                               220
65      Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
66      225                               230                               235                               240
67      Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
68                               245                               250                               255

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69      <210> SEQ ID NO 3
70      <211> LENGTH: 20
71      <212> TYPE: DNA
72      <213> ORGANISM: Homo sapiens
73      <400> SEQUENCE: 3
74      ttytgymgaa artayaaycc
75      <210> SEQ ID NO 4
76      <211> LENGTH: 20
77      <212> TYPE: DNA
78      <213> ORGANISM: Homo sapiens
79      <400> SEQUENCE: 4
80      ttytcstsca htggtggaca
81      <210> SEQ ID NO 5
82      <211> LENGTH: 20
83      <212> TYPE: DNA
84      <213> ORGANISM: Homo sapiens
85      <400> SEQUENCE: 5
86      cccargswrc aggtytttrca
87      <210> SEQ ID NO 6
88      <211> LENGTH: 20
89      <212> TYPE: DNA
90      <213> ORGANISM: Homo sapiens
91      <400> SEQUENCE: 6
92      ttytgrtcrtr traatgttcc
93      <210> SEQ ID NO 7
94      <211> LENGTH: 25

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95 <212> TYPE: DNA
96 <213> ORGANISM: Homo sapiens
97 <400> SEQUENCE: 7
98 aataagcttt gctagtatca tacct 25
99 <210> SEQ ID NO 8
100 <211> LENGTH: 30
101 <212> TYPE: DNA
102 <213> ORGANISM: Homo sapiens
103 <400> SEQUENCE: 8
104 ttaagatctc tgcggagagt gtcctggctc 30
105 <210> SEQ ID NO 9
106 <211> LENGTH: 2350
107 <212> TYPE: DNA
108 <213> ORGANISM: Mus musculus
109 <220> FEATURE:
110 <221> NAME/KEY: unsure
111 <222> LOCATION: (1253)...(1255)
112 <223> OTHER INFORMATION: (a or g or c or t/u)
113 <400> SEQUENCE: 9
114 atgtccatga actgctgagt ggataaacag cacgggatat ctctgtctaa aggaatatta 60
115 ctacaccagg aaaaggacac attcgacaac aggaaaggag cctgtcacag aaaaccacag 120
116 tgtcctgtgc atgtgacatt tcgccatggg aaacaactgt tacaacgtgg tggtcattgt 180
117 gctgctgcta gtgggctgtg agaagggtgg agcctgtcag aactcctgtg ataactgtca 240
118 gcctggtact ttctgcagaa aatacaatcc agtctgcaag agctgccctc caagtacctt 300
119 ctccagcata ggtggacagc cgaactgtaa catctgcaga gtgtgtgcag gctatttcag 360
120 gttcaagaag ttttgcctct ctaccacaa cgcggagtgt gagtgcattg aaggattcca 420
121 ttgcttgggg ccacagtgc cagatgtga aaaggactgc aggcctggcc aggagctaac 480
122 gaagcagggg tgcaaaacct gtagcttggg aacattttaa gaccagaacg gtactggcgt 540
123 ctgtcgaccc tggacgaact gctctctaga cggaaaggtct gtgcttaaga cggggaccac 600
124 ggagaaggac gtggtgtgtg gacccctgt ggtgagcttc tctcccagta ccaccatttc 660
125 tgtgactcca gagggaggac caggagggca ctccctgcag gtccttacct tgttcctggc 720
126 gctgacatcg gctttgctgc tggccctgat cttcattact ctccgtttct ctgtgtcaa 780
127 atggatcagg aaaaaattcc cccacatatt caagcaacca tttaagaaga cactggagc 840
128 agctcaagag gaagatgctt gtagctgccg atgtccacag gaagaagaag gaggaggagg 900
129 aggctatgag ctgtgatgta ctatcctagg agatgtgtgg gccgaaaccg agaagcacta 960
130 ggacccacc atcctgtgga acagcacaag caacccacc accctgttct tacacatcat 1020
131 cctagatgat gtgtgggcgc gcacctcatc caagtctctt ctaacgctaa catatttgtc 1080
132 ttacctttt ttaaattctt ttttaaattt aaattttatg tgtgtgagtg ttttgctgc 1140
133 ctgtatgcac acgtgtgtgt gtgtgtgtgt gtgacactcc tgatgcctga ggaggtcaga 1200
134 agacaaaggg ttggttccat aagaactgga gttatggatg gctgtgagcc ggnngatag 1260
135 gtcgggacgg agacctgtct tcttatttta acgtgactgt ataataaaaa aaaaatgata 1320
136 tttcgggaat ttagagatt gtccgtgacac ccttctagtt aatgatctaa gaggaattgt 1380
137 tgatacgtag tatactgtat atgtgtatgt atatgtatat gtatatataa gactctttta 1440
138 ctgtcaaagt caacctagag tgtctggtta ccaggtcaat tttattggac attttacgtc 1500
139 acacacacac acacacacac acacacacgt ttatactacg tactgttatc ggtattctac 1560
140 gtcataataat gggatagggt aaaaggaaac caaagagtga gtgatattat tgtggagggtg 1620
141 acagactacc ccttctgggt acgtagggac agacctcctt cggactgtct aaaactcccc 1680
142 ttagaagtct cgtcaagttc ccggacgaag aggacagagg agacacagtc cgaagagtta 1740
143 ttttccggc aaatcctttc cctgtttcgt gacactccac cccttgtgga cacttgagtg 1800
144 tcaccttgc gccggaaggt caggtggtac ccgtctgtag gggcggggag acagagccgc 1860

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145      ggggggagcta cgagaatcga ctcacagggc gccccgggct tcgcaaatga aactttttta      1920
146      atctcacaag tttcgtccgg gctcggcgga cctatggcgt cgatccttat taccttatcc      1980
147      tggcgccaag ataaaaacaac caaaagcctt gactccggta ctaattctcc ctgccggccc      2040
148      ccgtaagcat aacgcggcga tctccacttt aagaacctgg ccgcgttctg cctgggtctcg      2100
149      ctttcgtaaa cggttcttac aaaagtaatt agttcttgct ttcagcctcc aagcttctgc      2160
150      tagtctatgg cagcatcaag gctggtatatt gctacggctg accgctacgc cgccgcaata      2220
151      aggggtactgg gcggcccgtc gaaggccctt tggtttcaga aaccaaggc cccctcata      2280
152      ccaacgtttc gactttgatt cttgccggta cgtgggtggtg ggtgccttag ctctttctcg      2340
153      atagttagac                                     2350

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154 <210> SEQ ID NO 10

155 <211> LENGTH: 256

156 <212> TYPE: PRT

157 <213> ORGANISM: Mus musculus

158 <400> SEQUENCE: 10

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159      Met Gly Asn Asn Cys Tyr Asn Val Val Val Ile Val Leu Leu Leu Val
160      1          5          10          15
161      Gly Cys Glu Lys Val Gly Ala Val Gln Asn Ser Cys Asp Asn Cys Gln
162      20          25          30
163      Pro Gly Thr Phe Cys Arg Lys Tyr Asn Pro Val Cys Lys Ser Cys Pro
164      35          40          45
165      Pro Ser Thr Phe Ser Ser Ile Gly Gly Gln Pro Asn Cys Asn Ile Cys
166      50          55          60
167      Arg Val Cys Ala Gly Tyr Phe Arg Phe Lys Lys Phe Cys Ser Ser Thr
168      65          70          75          80
169      His Asn Ala Glu Cys Glu Cys Ile Glu Gly Phe His Cys Leu Gly Pro
170      85          90          95
171      Gln Cys Thr Arg Cys Glu Lys Asp Cys Arg Pro Gly Gln Glu Leu Thr
172      100         105         110
173      Lys Gln Gly Cys Lys Thr Cys Ser Leu Gly Thr Phe Asn Asp Gln Asn
174      115         120         125
175      Gly Thr Gly Val Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Arg
176      130         135         140
177      Ser Val Leu Lys Thr Gly Thr Thr Glu Lys Asp Val Val Cys Gly Pro
178      145         150         155         160
179      Pro Val Val Ser Phe Ser Pro Ser Thr Thr Ile Ser Val Thr Pro Glu
180      165         170         175
181      Gly Gly Pro Gly Gly His Ser Leu Gln Val Leu Thr Leu Phe Leu Ala
182      180         185         190
183      Leu Thr Ser Ala Leu Leu Leu Ala Leu Ile Phe Ile Thr Leu Leu Phe
184      195         200         205
185      Ser Val Leu Lys Trp Ile Arg Lys Lys Phe Pro His Ile Phe Lys Gln
186      210         215         220
187      Pro Phe Lys Lys Thr Thr Gly Ala Ala Gln Glu Glu Asp Ala Cys Ser
188      225         230         235         240
189      Cys Arg Cys Pro Gln Glu Glu Glu Gly Gly Gly Gly Tyr Glu Leu
190      245         250         255

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191 <210> SEQ ID NO 11

192 <211> LENGTH: 24

193 <212> TYPE: PRT

194 <213> ORGANISM: Homo sapiens

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195 <220> FEATURE:
196 <221> NAME/KEY: ZN_FING
197 <222> LOCATION: 2...3, 5...13, 15...17, 19...21, 23
198 <223> OTHER INFORMATION: Putative zinc finger structure
199 <400> SEQUENCE: 11
W- 200 Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa
W- 201 1 5 10 15
202 Xaa His Xaa Xaa Xaa Cys Xaa Cys
203 20
204 <210> SEQ ID NO 12
205 <211> LENGTH: 12
206 <212> TYPE: PRT
207 <213> ORGANISM: Homo sapiens
208 <400> SEQUENCE: 12
209 Leu Gln Asp Pro Cys Ser Asn Cys Pro Ala Gly Thr
210 1 5 10

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VERIFICATION SUMMARY
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| Line | ? Error/Warning | Original Text |
|------|---------------------------------------|---|
| 134 | W "N" or "Xaa" used: Feature required | agacaaaggg ttggttccat aagaactgga gttatgga |
| 200 | W "N" or "Xaa" used: Feature required | Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa X |
| 202 | W "N" or "Xaa" used: Feature required | Xaa His Xaa Xaa Xaa Cys Xaa Cys |